AMENDMENTS TO THE CLAIMS

This listing of the claims will replace all prior versions, and listings, of claims in this application.

Listing of Claims

1. (Currently Amended) A method for identifying a compound which modulates an interaction between a first and a second polypeptide comprising:

(a) contacting a cell having a first polypeptide comprising a binding portion of a KRC polypeptide and a second polypeptide comprising a binding portion of a polypeptide selected from the group consisting of: ~~Jun,~~ GATA3, SMAD, or Runx2 in the presence and the absence of a test compound; and

(b) determining the degree of interaction between the first and the second polypeptide in the presence and the absence of the test compound,

to thereby identify a compound which modulates an interaction between a first and a second polypeptide.

2. (Original) The method of claim 1, wherein the first polypeptide comprises at least one KRC zinc finger domain.

3. (Canceled)

4. (Original) The method of claim 1, wherein the second polypeptide is a SMAD2 polypeptide.

5. (Original) The method of claim 1, wherein the second polypeptide is a SMAD3 polypeptide.

6 (Original) The method of claim 1, wherein the first polypeptide is derived from an exogenous source.

7. (Original) The method of claim 1, wherein the second polypeptide is derived from an exogenous source.

8. (Original) The method of claim 1, wherein the cell is a yeast cell.

9. (Original) The method of claim 8, wherein determining the ability of the test compound to modulate the interaction of the first polypeptide and the second polypeptide comprises determining the ability of the compound to modulate growth of the yeast cell on nutritionally selective media.

10 (Original) The method of claim 8, wherein determining the ability of the test compound to modulate the interaction of the first polypeptide and the second polypeptide comprises determining the ability of the compound to modulate expression of a reporter gene in the yeast cell.

11. (Original) The method of claim 1, wherein determining the ability of the test compound to modulate the interaction of the first polypeptide and the second polypeptide comprises determining the ability of the test compound to modulate the coimmunoprecipitation of the first polypeptide and the second polypeptide.

12. (Original) The method of claim 1, wherein determining the ability of the test compound to modulate the interaction of the first polypeptide and the second polypeptide comprises determining the ability of the test compound to modulate signaling via a signal transduction pathway involving KRC in the cell.

13 (Original) The method of claim 12, wherein at least one of TNFα production, IL-2 production, AP-1 activity, Ras and Rac activity, actin polymerization, ubiquitination of AP-1, ubiquitination of TRAF, ubiquitination of Runx2, degradation of c-Jun, degradation of c-Fos degradation of SMAD, degradation of Runx2, degradation of GATA3, GATA3 expression, Th2 cell differentiation, Th2 cytokine production, IgA production, GLα transcription (Igα chain germline transcription), and/or osteocalcin gene transcription is measured.

14. (Original) The method of claim 12, wherein ubiquitination or degradation of c-fos, c-Jun, SMAD3, GATA3 or Runx2 is measured.

15. (Original) The method of claim 12, wherein AP-1, TRAF2 or Runx2 ubiquitination is measured.

16. (Original) The method of claim 1, wherein the binding of first and second polypeptide is inhibited.

17. (Original) The method of claim 1, wherein the binding of first and second polypeptide is stimulated.

18. (Original) A method of identifying a compound that modulates a mammalian KRC biological activity comprising:

(a) contacting cells deficient in KRC or a molecule in a signaling pathway involving KRC with a test compound; and

(b) determining the effect of the test compound on the KRC biological activity, the test compound being identified as a modulator of the biological activity based on the ability of the test compound to modulate the biological activity in the cells deficient in KRC or a molecule in a signaling pathway involving KRC to thereby identify a compound that modulates a mammalian KRC biological activity.

19. (Original) The method of claim 18, wherein the biological activity of KRC is selected from the group consisting of modulation of: modulation of a TGFβ signaling pathway, modulation of ubiquitination of AP-1, modulation of ubiquitination of TRAF, modulation of ubiquitination of Runx2, modulation of the degradation of c-Jun, modulation of the degradation of c-Fos, modulation of degradation of SMAD, modulation of degradation of Runx, modulation of degradation of GATA3, modulation of GATA3 expression, modulation of Th2 cell differentiation, modulation of Th2 cytokine production, modulation of IgA production, modulation of GLα transcription, or modulation of osteocalcin gene transcription.

20. (Original) The method of claim 18, wherein the cells are in a non-human animal deficient in KRC or a molecule in a signal transduction pathway involving KRC and the cells are contacted with the test compound by administering the test compound to the animal.

21. (Currently Amended) A method of identifying compounds useful in modulating a biological activity of mammalian KRC comprising:

a) providing an indicator composition comprising mammalian KRC or a molecule in a signal transduction pathway involving KRC;

b) contacting the indicator composition with each member of a library of test compounds;

c) selecting from the library of test compounds a compound of interest that modulates a biological activity of KRC or the molecule in a signal transduction pathway involving KRC; to thereby identify a compound that modulates a biological activity of mammalian KRC, wherein the biological activity of KRC is selected from the group consisting of: ~~modulation of a TGFβ signaling pathway, modulation of ubiquitination of AP-1, modulation of ubiquitination of TRAF,~~ modulation of ubiquitination of Runx2, ~~modulation of the degradation of c-Jun, modulation of the degradation of c-Fos,~~ modulation of degradation of SMAD, modulation of degradation of Runx, modulation of degradation of GATA3, modulation of GATA3 expression, modulation of Th2 cell differentiation, modulation of Th2 cytokine production, modulation of IgA production, modulation of GLα transcription, and modulation of osteocalcin gene transcription.

22. (Currently Amended) The method of claim 21, wherein the indicator composition is a cell that expresses KRC, and at least one molecule selected from the group consisting of: ~~c-Jun, c-Fos, AP-1,~~ GATA3, SMAD, and Runx2 protein.

23. (Original) The method of claim 21, wherein the indicator composition is a cell free composition.

24.-45. (Canceled)

46. (Original) A non-human animal, in which the gene encoding the KRC gene is misexpressed.

47. (Original) The animal of claim 46, wherein the animal is a transgenic animal.

48. (Original) The animal of claim 47, wherein the transgenic animal is a mouse.

49. (Original) The animal of claim 46, wherein the KRC gene is disrupted by removal of DNA encoding all or part of the KRC protein.

50. (Original) The animal of claim 49, wherein the animal is homozygous for the disrupted gene.

51. (Original) The animal of claim 49, wherein the animal is heterozygous for the disrupted gene.

52. (Original) The animal of claim 46, wherein the animal is a transgenic mouse with a transgenic disruption of the KRC gene.

53. (Original) The animal of claim 52, wherein the disruption is an insertion or deletion.

54. (Original) A transgenic mouse comprising in its genome an exogenous DNA molecule that functionally disrupts a KRC gene of said mouse, wherein the mouse exhibits a phenotype characterized by impaired Th2 cell development, decreased Th2 cytokine production, impaired TGFβR signaling in B cells, decreased IgA secretion and decreased transcription of the GLα gene, relative to a wildtype mouse.